

BLAST

Basic Local Alignment Search Tool

- Your search parameters were adjusted to search for a short input sequence.

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Protein Sequence (8 letters)

residues 66-73 of SEQ ID NO: 12

Results for: lcl|87188 None(8aa)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|87188

lcl|87188

Description

None

Molecule type

amino acid

Query Length

8

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

Program

BLASTP 2.2.22+ [Citation](#)

Reference

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402.

Other reports: [Search Summary](#) [\[Taxonomy reports\]](#) [\[Multiple alignment\]](#) [NEW](#)

Search Parameters

Program	blastp
Word size	2
Expect value	200000
Hitlist size	100
Gapcosts	9,1
Matrix	PAM30
Threshold	11
Filter string	F
Genetic Code	1
Window Size	40

Database

Posted date	Jan 3, 2010 5:44 PM
Number of letters	3,505,793,397
Number of sequences	10,274,250
Entrez query	none

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	0.345924	0.294
K	0.292556	0.11
H	1.73538	0.61

Results Statistics

Length adjustment 0
Effective length of query 8
Effective length of database 3505793397
Effective search space 28046347176
Effective search space used 28046347176

Graphic Summary

Show Conserved Domains

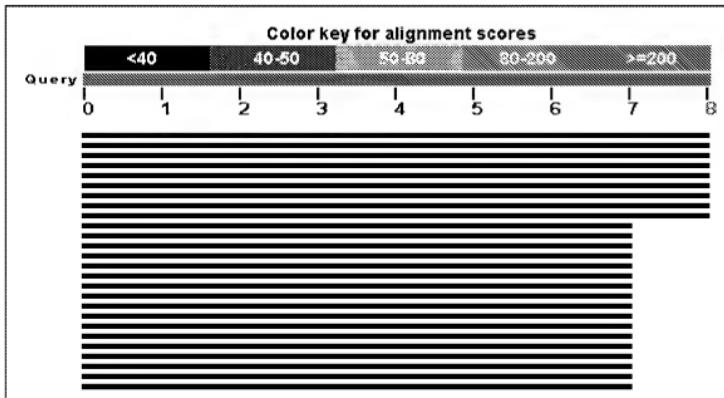
No putative conserved domains have been detected

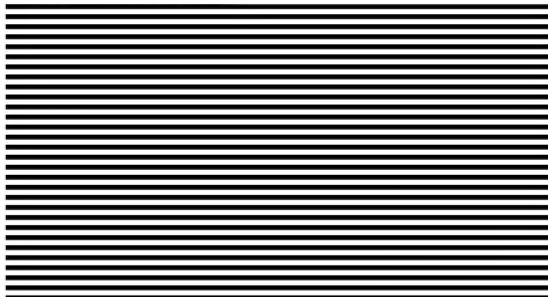


Distribution of 100 Blast Hits on the Query Sequence



An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.





XXXXXXXXXXXX

Descriptions

E	Score	
Sequences producing significant alignments:	(Bits)	Value
ref XP_051778582.1 hypothetical protein STA4A_07162 [Streptomyces sp. 100-162]	25.2	708
ref XP_001393186.1 hypothetical protein An08g10820 [Aspergillus fumigatus AF2937]	25.2	708
ref EP_01461905.1 beta-lactamase [Stigmella auranticae DW4]	25.2	708
gb IARD13661.1 surface antigen [Hepatitis B virus]	25.2	708
ref EP_04389235.1 bifunctional protein [Rhodococcus erythropolis M17]	24.9	949
ref YK_002764635.1 wax ester synthase/diacylglycerol acyltransferase [Mycobacterium smegmatis MC2 155]	24.8	949
gb EEE28299.1 conserved hypothetical protein [Toxoplasma gondii 3D7]	24.8	949
gb EEE20499.1 conserved hypothetical protein [Toxoplasma gondii 3D7]	24.8	949
ref NP_002370822.1 hypothetical protein TGME49_015010 [Toxoplasma gondii 3D7]	24.8	949
gb ACQ92751.1 S protein [Hepatitis B virus]	24.4	1274
gb ACQ92751.1 middle S protein [Hepatitis B virus]	24.4	1274
gb ACQ92750.1 large S protein [Hepatitis B virus]	24.4	1274
ref EP_04859486.1 conserved hypothetical protein [Ruminococcus sp. 100-162]	24.4	1274
gb IBAW84154.1 hepatitis B surface antigen [Hepatitis B virus]	24.4	1274
gb IBAW84102.1 hepatitis B surface antigen [Hepatitis B virus]	24.4	1274
gb IBAW82930.1 hepatitis B surface antigen [Hepatitis B virus]	24.4	1274
gb ACJ66248.1 middle S protein [Hepatitis B virus]	24.4	1274
gb ACJ66247.1 large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66246.1 S protein [Hepatitis B virus]	24.4	1274
gb ACJ66244.1 middle S protein [Hepatitis B virus]	24.4	1274
gb ACJ66240.1 large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66233.1 large S protein [Hepatitis B virus]	24.4	1274
gb NCJ66228.1 S protein [Hepatitis B virus]	24.4	1274
gb MCJ66227.1 middle S protein [Hepatitis B virus]	24.4	1274
gb MCJ66226.1 large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66213.1 middle S protein [Hepatitis B virus]	24.4	1274
gb ACJ66212.1 large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66207.1 S protein [Hepatitis B virus]	24.4	1274
gb ACJ66206.1 middle S protein [Hepatitis B virus]	24.4	1274
gb ACJ66205.1 large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66184.1 middle S protein [Hepatitis B virus]	24.4	1274
gb NCJ66185.1 large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66136.1 middle S protein [Hepatitis B virus] >gb ACJ66136.1	24.4	1274
gb MCJ66135.1 large S protein [Hepatitis B virus] >gb ACJ66135.1	24.4	1274
gb NCJ66130.1 S protein [Hepatitis B virus]	24.4	1274
gb ACJ66129.1 middle S protein [Hepatitis B virus]	24.4	1274
gb ACJ66128.1 large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66127.1 large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66096.1 S protein [Hepatitis B virus]	24.4	1274
gb ACJ66095.1 large S protein [Hepatitis B virus]	24.4	1274
gb ACJ66081.1 large S protein [Hepatitis B virus] >gb ACJ66081.1	24.4	1274
gb ACJ66080.1 S protein [Hepatitis B virus]	24.4	1274
gb ACJ66005.1 middle S protein [Hepatitis B virus]	24.4	1274
gb ACJ66004.1 large S protein [Hepatitis B virus]	24.4	1274
gb NCJ65907.1 middle S protein [Hepatitis B virus]	24.4	1274
gb MCJ65906.1 large S protein [Hepatitis B virus]	24.4	1274
gb ACJ65905.1 S protein [Hepatitis B virus]	24.4	1274
gb ACJ65904.1 middle S protein [Hepatitis B virus]	24.4	1274
gb ACJ65903.1 large S protein [Hepatitis B virus]	24.4	1274
ref YF_002963339.1 putative methyltransferase [Methylobacter sp. 100-162]	24.4	1274
gb ACP66198.1 large S protein [Hepatitis B virus]	24.4	1274
gb ACP66182.1 large S protein [Hepatitis B virus]	24.4	1274
gb ACP66182.1 large S protein [Hepatitis B virus]	24.4	1274
gb ACP66180.1 large S protein [Hepatitis B virus]	24.4	1274
gb ACR66170.1 large S protein [Hepatitis B virus]	24.4	1274
gb ACR66160.1 large S protein [Hepatitis B virus]	24.4	1274

gb ACR6153..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACR6138..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACR6129..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACR6123..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACR6597..11	large S protein [Hepatitis B virus] >gb ACR661...	24.4	1274
gb ACR6604..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACP6608..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACP6602..11	large S protein [Hepatitis B virus] >gb ACR660...	24.4	1274
gb ACP6601..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACR6596..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACR6595..11	large S protein [Hepatitis B virus] >gb ACR661...	24.4	1274
gb ACR6596..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACR6594..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACR6594..11	large S protein [Hepatitis B virus] >gb ACR659...	24.4	1274
gb ACR6594..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACR6593..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACR6592..11	large S protein [Hepatitis B virus] >gb ACR660...	24.4	1274
gb ACR6592..11	large S protein [Hepatitis B virus] >gb ACR660...	24.4	1274
gb ACP6592..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACP6593..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACR6589..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACR6589..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACR6588..11	large S protein [Hepatitis B virus] >gb ACR660...	24.4	1274
gb ACR6588..11	large S protein [Hepatitis B virus] >gb ACR660...	24.4	1274
gb ACR6587..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACR6586..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACR6585..11	large S protein [Hepatitis B virus] >gb ACR660...	24.4	1274
gb ACP6585..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACP6584..11	large S protein [Hepatitis B virus] >gb ACR659...	24.4	1274
gb ACP6584..11	large S protein [Hepatitis B virus] >gb ACR660...	24.4	1274
gb ACP6583..11	large S protein [Hepatitis B virus] >gb ACR658...	24.4	1274
gb ACR6582..11	large S protein [Hepatitis B virus] >gb ACR658...	24.4	1274
gb ACP6584..11	large S protein [Hepatitis B virus] >gb ACR660...	24.4	1274
gb ACR6583..11	large S protein [Hepatitis B virus] >gb ACR658...	24.4	1274
gb ACR6582..11	large S protein [Hepatitis B virus] >gb ACR658...	24.4	1274
gb ACR6581..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACR6580..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACR6580..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACR6580..11	large S protein [Hepatitis B virus] >gb ACR658...	24.4	1274
gb ACR6580..11	large S protein [Hepatitis B virus] >gb ACR658...	24.4	1274
ref XP_002578293..11	Upstream stimulatory factor [Schistosoma ...	24.4	1274
gb ACP20704..11	S protein [Hepatitis B virus]	24.4	1274
gb ACP20703..11	middle S protein [Hepatitis B virus]	24.4	1274
gb ACP20700..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACP20564..11	S protein [Hepatitis B virus]	24.4	1274
gb ACP20563..11	middle S protein [Hepatitis B virus]	24.4	1274
gb ACP20560..11	large S protein [Hepatitis B virus]	24.4	1274
gb ACP20413..11	S protein [Hepatitis B virus]	24.4	1274
gb ACP20412..11	middle S protein [Hepatitis B virus]	24.4	1274
gb ACP20411..11	large S protein [Hepatitis B virus]	24.4	1274

Alignments Select All Get selected sequences Distance tree of results Multiple alignment NEW

>ref|ZP_05477858..1| hypothetical protein StAA4_07162 [Streptomyces sp. AA4]
Length=241

Score = 25.2 bits (52), Expect = 708
Identities = 7/8 (87%), Positives = 8/8 (100%), Gaps = 0/8 (0%)

Query 1 PLIPGSTR 8
Sbjct 70 PLIPG+TR 77

>ref|XP_001393186..1| C hypothetical protein An08g10820 [Aspergillus niger]
emb|CAK45755..1| C unnamed protein product [Aspergillus niger]
Length=489

GENE ID: 4983396 An08g10820 | hypothetical protein

[Aspergillus niger CBS 513.88] (10 or fewer PubMed links)

Score = 25.2 bits (52), Expect = 708
Identities = 7/8 (87%), Positives = 8/8 (100%), Gaps = 0/8 (0%)

Query 1 PLIPGSTR 8
PLIPG+TR
Sbjct 327 PLIPGTTTR 334

>**ref|ZP_01461905.1|** beta-lactamase [Stigmatella aurantiaca DW4/3-1]
>**gb|EAU67348.1|** beta-lactamase [Stigmatella aurantiaca DW4/3-1]
Length=392

Score = 25.2 bits (52), Expect = 708
Identities = 7/8 (87%), Positives = 8/8 (100%), Gaps = 0/8 (0%)

Query 1 PLIPGSTR 8
PL+PGSTR
Sbjct 294 PLVPGSTR 301

>**gb|AAD13661.1|** surface antigen [Hepatitis B virus]
Length=226

Score = 25.2 bits (52), Expect = 708
Identities = 7/8 (87%), Positives = 8/8 (100%), Gaps = 0/8 (0%)

Query 1 PLIPGSTR 8
PLIPG+TR
Sbjct 108 PLIPGTTTR 115

>**ref|ZP_04388235.1|** bifunctional protein [Rhodococcus erythropolis SK121]
>**gb|BEN84692.1|** bifunctional protein [Rhodococcus erythropolis SK121]
Length=458

Score = 24.8 bits (51), Expect = 949
Identities = 7/8 (87%), Positives = 8/8 (100%), Gaps = 0/8 (0%)

Query 1 PLIPGSTR 8
PLIPGS+R
Sbjct 363 PLIPGSSR 370

>**ref|YP_002764633.1|** wax ester synthase/diacylglycerol acyltransferase [Rhodococcus erythropolis PR4]

>**dbj|BAH31894.1|** putative wax ester synthase/diacylglycerol acyltransferase [Rhodococcus erythropolis PR4]
Length=458

GENE ID: 7714817 RER_11860 | wax ester synthase/diacylglycerol acyltransferase [Rhodococcus erythropolis PR4] (10 or fewer PubMed links)

Score = 24.8 bits (51), Expect = 949
Identities = 7/8 (87%), Positives = 8/8 (100%), Gaps = 0/8 (0%)

Query 1 PLIPGSTR 8
PLIPGS+R
Sbjct 363 PLIPGSSR 370

>**gb|EEE28209.1|** conserved hypothetical protein [Toxoplasma gondii VEG]
Length=417

Score = 24.8 bits (51), Expect = 949
Identities = 7/8 (87%), Positives = 8/8 (100%), Gaps = 0/8 (0%)

Query 1 PLIPGSTR 8
PLIPGS+R
Sbjct 181 PLIPGSSR 188

>**gb|EEE20499.1|** conserved hypothetical protein [Toxoplasma gondii GT1]
Length=405

Score = 24.8 bits (51), Expect = 949
Identities = 7/8 (87%), Positives = 8/8 (100%), Gaps = 0/8 (0%)

Query 1 PLIPGSTR 8
PLIPGS+R
Sbjct 169 PLIPGSSR 176

>ref|XP_002370822.1| **G** hypothetical protein TGME49_015010 [Toxoplasma gondii ME49]
>gb|EEB03682.1| **G** hypothetical protein TGME49_015010 [Toxoplasma gondii ME49]
Length=405

GENE ID: 7900763 TGME49_015010 | hypothetical protein [Toxoplasma gondii ME49]

Score = 24.8 bits (51), Expect = 949
Identities = 7/8 (87%), Positives = 8/8 (100%), Gaps = 0/8 (0%)

Query 1 PLIPGSTR 8
PLIPGS+R
Sbjct 169 PLIPGSSR 176

>gb|ACQ82752.1| S protein [Hepatitis B virus]
Length=226

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
PLIPGST
Sbjct 108 PLIPGST 114

>gb|ACQ82751.1| middle S protein [Hepatitis B virus]
Length=281

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
PLIPGST
Sbjct 163 PLIPGST 169

>gb|ACQ82750.1| large S protein [Hepatitis B virus]
Length=400

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
PLIPGST
Sbjct 282 PLIPGST 288

>ref|ZP_04858486.1| conserved hypothetical protein [Ruminococcus sp. 5_1_39B_FAA]
>gb|EES75479.1| conserved hypothetical protein [Ruminococcus sp. 5_1_39B_FAA]
Length=146

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
PLIPGST
Sbjct 90 PLIPGST 96

>dbj|BAH84154.1| hepatitis B surface antigen [Hepatitis B virus]
Length=132

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
PLIPGST
Sbjct 69 PLIPGST 75

>dbj|BAH84102.1| hepatitis B surface antigen [Hepatitis B virus]
Length=132

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
PLIPGST
Sbjct 69 PLIPGST 75

>dbj|BAH83930.1| hepatitis B surface antigen [Hepatitis B virus]
Length=132

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
PLIPGST
Sbjct 69 PLIPGST 75

>gb|ACJ66248.1| middle S protein [Hepatitis B virus]
Length=281

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
PLIPGST
Sbjct 163 PLIPGST 169

>gb|ACJ66247.1| large S protein [Hepatitis B virus]
Length=400

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
PLIPGST
Sbjct 282 PLIPGST 288

>gb|ACJ66242.1| S protein [Hepatitis B virus]
Length=226

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
PLIPGST
Sbjct 108 PLIPGST 114

>gb|ACJ66241.1| middle S protein [Hepatitis B virus]
Length=281

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
PLIPGST
Sbjct 163 PLIPGST 169

>gb|ACJ66240.1| large S protein [Hepatitis B virus]
Length=400

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)

Query 1 PLIPGST 7
PLIPGST
Sbjct 282 PLIPGST 288

>gb|ACJ66233.1| large S protein [Hepatitis B virus]
Length=400

Score = 24.4 bits (50), Expect = 1274
Identities = 7/7 (100%), Positives = 7/7 (100%), Gaps = 0/7 (0%)